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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:01:42 ; Search time 55 Seconds  
(without alignments)  
30.823 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 40    | 100.0       | 6      | 5  | AAM48538 | Aam48538 Anti-infl |
| 2          | 40    | 100.0       | 6      | 5  | AAM48570 | Aam48570 Anti-infl |
| 3          | 40    | 100.0       | 6      | 6  | ADA61814 | Ada61814 NFkB esse |
| 4          | 40    | 100.0       | 6      | 6  | ADA61846 | Ada61846 NFkB esse |
| 5          | 40    | 100.0       | 7      | 5  | AAM48574 | Aam48574 Anti-infl |
| 6          | 40    | 100.0       | 7      | 6  | ADA61850 | Ada61850 NFkB esse |
| 7          | 40    | 100.0       | 8      | 5  | AAM48575 | Aam48575 Anti-infl |
| 8          | 40    | 100.0       | 8      | 5  | AAM48567 | Aam48567 Anti-infl |
| 9          | 40    | 100.0       | 8      | 6  | ADA61851 | Ada61851 NFkB esse |
| 10         | 40    | 100.0       | 9      | 5  | AAM48573 | Aam48573 Anti-infl |
| 11         | 40    | 100.0       | 9      | 5  | AAM48566 | Aam48566 Anti-infl |
| 12         | 40    | 100.0       | 9      | 5  | AAM48569 | Aam48569 Anti-infl |
| 13         | 40    | 100.0       | 9      | 5  | AAM48572 | Aam48572 Anti-infl |
| 14         | 40    | 100.0       | 9      | 6  | ADA61848 | Ada61848 NFkB esse |
| 15         | 40    | 100.0       | 9      | 6  | ADA61841 | Ada61841 NFkB esse |
| 16         | 40    | 100.0       | 9      | 6  | ADA61849 | Ada61849 NFkB esse |
| 17         | 40    | 100.0       | 9      | 6  | ADA61845 | Ada61845 NFkB esse |
| 18         | 40    | 100.0       | 9      | 6  | ADA61842 | Ada61842 NFkB esse |
| 19         | 40    | 100.0       | 10     | 5  | AAM48568 | Aam48568 Anti-infl |
| 20         | 40    | 100.0       | 10     | 5  | AAM48571 | Aam48571 Anti-infl |
| 21         | 40    | 100.0       | 10     | 6  | ADA61844 | Ada61844 NFkB esse |
| 22         | 40    | 100.0       | 10     | 6  | ADA61847 | Ada61847 NFkB esse |
| 23         | 40    | 100.0       | 11     | 5  | AAM48565 | Aam48565 Anti-infl |
| 24         | 40    | 100.0       | 11     | 6  | ADA61840 | Ada61840 NFkB esse |
| 25         | 40    | 100.0       | 11     | 6  | ADA61840 | Ada61840 NFkB esse |

|    |    |      |     |   |          |                    |
|----|----|------|-----|---|----------|--------------------|
| 26 | 37 | 92.5 | 33  | 4 | AAU21305 | Aau21305 Human nov |
| 27 | 37 | 92.5 | 103 | 2 | AAV06332 | Aay06332 Glioclast |
| 28 | 37 | 92.5 | 236 | 2 | AAV06363 | Aay06363 Glioclast |
| 29 | 37 | 92.5 | 236 | 3 | AAV84341 | Aay84341 Amino aci |
| 30 | 37 | 92.5 | 236 | 3 | AAV14876 | Aab14876 Glioclast |
| 31 | 37 | 92.5 | 236 | 5 | AAU77584 | Aau77584 G. roseum |
| 32 | 37 | 92.5 | 236 | 5 | AAU77428 | Aau77428 Glioclast |
| 33 | 37 | 92.5 | 274 | 5 | ABP65718 | Abp65718 Bifidobac |
| 34 | 37 | 92.5 | 597 | 4 | ABB62635 | Abb62635 Drosophil |
| 35 | 37 | 92.5 | 885 | 4 | AAU33594 | Aau33594 Pseudomon |
| 36 | 37 | 92.5 | 885 | 6 | ABU15648 | Abu15648 Protein e |
| 37 | 36 | 90.0 | 6   | 5 | ABB08727 | Abb08727 Mutated I |
| 38 | 36 | 90.0 | 6   | 5 | ABB08728 | Abb08728 Mutated I |
| 39 | 36 | 90.0 | 6   | 5 | AAM48537 | Aam48537 Anti-infl |
| 40 | 36 | 90.0 | 6   | 5 | AAM48548 | Aam48548 Anti-infl |
| 41 | 36 | 90.0 | 6   | 5 | AAM48559 | Aam48559 Anti-infl |
| 42 | 36 | 90.0 | 6   | 5 | AAM48509 | Aam48509 NBD mutan |
| 43 | 36 | 90.0 | 6   | 5 | AAM48510 | Aam48510 NBD mutan |
| 44 | 36 | 90.0 | 6   | 5 | AAM48536 | Aam48536 Anti-infl |
| 45 | 36 | 90.0 | 6   | 6 | ABU08420 | Abu08420 Human NEM |

ALIGNMENTS

|  |                          |
|--|--------------------------|
| RESULT 1   |                          |
| ID AAM48538  | standard; peptide; 6 AA. |
| AC AAM48538;   |                          |
| DT 20-MAR-2002   | (first entry)            |
| DE Anti-inflammatory peptide SEQ ID NO 41.                                   |                          |
| XX   |                          |
| KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;    |                          |
| KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;       |                          |
| KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  |                          |
| KW antiallergic; membrane translocation domain; NEMO binding domain; eczema; |                          |
| KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;      |                          |
| KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;         |                          |
| KW autoimmune disorder; multiple sclerosis; transplant rejection;            |                          |
| KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;      |                          |
| KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.                   |                          |
| XX   |                          |
| OS Synthetic.  |                          |
| XX   |                          |
| PN WO200183554-A2.   |                          |
| XX   |                          |
| PD 08-NOV-2001.  |                          |
| XX   |                          |
| PE 02-MAY-2001; 2001WO-US014346.   |                          |
| XX   |                          |
| PR 02-MAY-2000; 2000US-0201261P.   |                          |
| PR 22-AUG-2000; 2000US-00643260.   |                          |
| XX   |                          |
| PA (PRAE-) PRAECIS PHARM INC.  |                          |
| PA (UYVA ) UNIV YALE.  |                          |
| PI May MJ, Ghosh S, Findeis MA, Phillips K;                                  |                          |
| XX   |                          |
| DR WPI; 2002-121889/16.  |                          |
| XX   |                          |
| PT Novel antiinflammatory compound comprising membrane translocation domain  |                          |
| PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB |                          |
| PT activation, and for treating asthma, lung inflammation, psoriasis.        |                          |
| XX   |                          |
| PS Claim 6; Page 61; 88pp; English.  |                          |
| XX   |                          |
| CC The invention relates to an antiinflammatory compound (especially         |                          |
| CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620- |                          |
| CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid       |                          |
| CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The       |                          |

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, CC antirheumatic, antiarthritic, osteopathic, antibacterial, CC immunosuppressive, dermatological, neuroprotective, nootropic, CC antiatherosclerotic, virucide and antiallergic activity. The compounds CC act as selective inhibitors of cytokine-mediated NFkappaB activation by CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding CC domain that results in inhibition of IKKbeta kinase activation and CC subsequent decreased phosphorylation of IkappaB. The compounds are useful CC for treating inflammatory disorders, e.g. asthma, lung inflammation or CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; CC viral infections; and ataxia telangiectasia. The compounds are also CC useful for treating pro-inflammatory responses such as allergies, CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, CC sunburn, aging and arthritis

SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
Db 1 ADMSWA 6

RESULT 2  
AAM48570  
ID AAM48570 standard; peptide; 6 AA.

AC AAM48570;  
DT 20-MAR-2002 (first entry)  
DE Anti-inflammatory peptide SEQ ID NO 73.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.  
PR 22-AUG-2000; 2000US-00643260.

PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis

SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
Db 1 ADMSWA 6

RESULT 3  
ADA61814  
ID ADA61814 standard; peptide; 6 AA.

AC ADA61814;  
DT 20-NOV-2003 (first entry)  
DE NFkB essential modulator (NEMO) binding peptide #14.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.

OS Unidentified.

XX US2003054999-A1.

XX PD 20-MAR-2003.

PF 02-MAY-2001; 2001US-00847946.

PR 02-MAY-2000; 2000US-0201261P.

PA (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.

PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

DR WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 6; Page 23; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
CC  
XX  
SQ Sequence 6 AA;  
SQ  
Query Match 100.0%; Score 40; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADWSWA 6  
Db 1 ADWSWA 6  
RESULT 4  
ADA61846  
ID ADA61846 standard; peptide; 6 AA.  
XX  
AC ADA61846;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #46.  
XX  
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytosstatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
XX (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G,  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.

XX Claim 6; Page 23; 37pp; English.  
PS  
XX  
CC The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
CC  
XX  
SQ Sequence 6 AA;  
SQ  
Query Match 100.0%; Score 40; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADWSWA 6  
Db 1 ADWSWA 6  
RESULT 5  
AAM48574  
ID AAM48574 standard; peptide; 7 AA.  
XX  
AC AAM48574;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 77.  
XX  
XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K,  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappab  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytosstatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 1 ADWSWA 6

RESULT 6  
ADA61850  
ID ADA61850 standard; peptide; 7 AA.

AC ADA61850;

XX 20-NOV-2003 (first entry)

DE NFkB essential modulator (NEMO) binding peptide #50.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytosstatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
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XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
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XX The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
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CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 1 ADWSWA 6

RESULT 7  
AAM48575  
ID AAM48575 standard; peptide; 8 AA.

XX AAM48575;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 78.

XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

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XX May MJ, Ghosh S, Findels MA, Phillips K;

XX WPI; 2002-121889/16.

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PT activation, and for treating asthma, lung inflammation, psoriasis.

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XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytosstatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,



CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

RESULT 8  
AAM48567  
ID AAM48567 standard; peptide; 8 AA.

AC AAM48567;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 70.

XX Antinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cyostatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 3 ADMSWA 8

RESULT 9  
ADA61851  
ID ADA61851 standard; peptide; 8 AA.

AC ADA61851;

DT 20-NOV-2003 (first entry)

DE NFkB essential modulator (NEMO) binding peptide #51.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cyostatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 6; Page 23; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 8 AA;  
  
QY Query Match 100.0%; Score 40; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 1 ADWSWA 6  
  
RESULT 10  
ADA61843  
ID ADA61843 standard; peptide; 8 AA.  
XX  
AC ADA61843;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #43.  
XX  
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 6; Page 23; 37pp; English.  
XX

CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 8 AA;  
  
QY Query Match 100.0%; Score 40; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 3 ADWSWA 8  
  
RESULT 11  
AAM48573  
ID AAM48573 standard; peptide; 9 AA.  
XX  
AC AAM48573;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 76.  
XX  
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappab  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of Ikappab. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||  
Db 2 ADMSWA 7

## RESULT 12

AAM48566  
ID AAM48566 standard; peptide; 9 AA.

AC AAM48566;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 69.

XX  
KW Anti-inflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

PA (PRAE-) PRAECTIS PHARM INC.  
(UYVA ) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappab  
PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cyostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappab activation by  
CC blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of Ikappab. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||  
Db 1 ADMSWA 6

## RESULT 13

AAM48569  
ID AAM48569 standard; peptide; 9 AA.

AC AAM48569;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 72.

XX  
KW Anti-inflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

PA (PRAE-) PRAECTIS PHARM INC.  
(UYVA ) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappab  
PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 6; Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
CC  
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 1 ADWSMA 6

RESULT 14  
AAM48572  
ID AAM48572 standard; peptide; 9 AA.

AC AAM48572;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 75.

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121869/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 88pp; English.  
PS  
XX

CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-  
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The  
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,  
CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, nootropic,  
CC antiatherosclerotic, virucide and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
CC  
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
Db 3 ADWSMA 8

RESULT 15  
ADA61848  
ID ADA61848 standard; peptide; 9 AA.

AC ADA61848;

DT 20-NOV-2003 (first entry)

DE NFkB essential modulator (NEMO) binding peptide #48.

KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;  
KW antirheumatic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYM/) MAY, M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX



PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.

PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.

XX  
PS Claim 6; Page 23; 37pp; English.

XX  
CC The invention describes an anti-inflammatory compound comprising (I). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||  
Db 3 ADMSWA 8

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Job time : 56 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:08:54 ; Search time 42 Seconds  
(without alignments)  
39.496 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | length | ID                   | Description       |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1          | 40    | 100.0       | 6      | 10 US-09-847-946A-41 | Sequence 41, Appl |
| 2          | 40    | 100.0       | 6      | 10 US-09-847-946A-73 | Sequence 73, Appl |
| 3          | 40    | 100.0       | 7      | 10 US-09-847-946A-77 | Sequence 77, Appl |
| 4          | 40    | 100.0       | 8      | 10 US-09-847-946A-70 | Sequence 70, Appl |
| 5          | 40    | 100.0       | 8      | 10 US-09-847-946A-78 | Sequence 78, Appl |
| 6          | 40    | 100.0       | 9      | 10 US-09-847-946A-69 | Sequence 69, Appl |
| 7          | 40    | 100.0       | 9      | 10 US-09-847-946A-72 | Sequence 72, Appl |
| 8          | 40    | 100.0       | 9      | 10 US-09-847-946A-75 | Sequence 75, Appl |
| 9          | 40    | 100.0       | 9      | 10 US-09-847-946A-76 | Sequence 76, Appl |
| 10         | 40    | 100.0       | 10     | 10 US-09-847-946A-71 | Sequence 71, Appl |
| 11         | 40    | 100.0       | 10     | 10 US-09-847-946A-74 | Sequence 74, Appl |
| 12         | 40    | 100.0       | 11     | 10 US-09-847-946A-68 | Sequence 68, Appl |
| 13         | 37    | 92.5        | 236    | 12 US-10-441-625-17  | Sequence 17, Appl |
| 14         | 37    | 92.5        | 236    | 14 US-10-441-626-17  | Sequence 17, Appl |
| 15         | 37    | 92.5        | 885    | 9 US-09-815-242-5090 | Sequence 5090, Ap |

|    |    |      |     |    |                      |                   |
|----|----|------|-----|----|----------------------|-------------------|
| 16 | 37 | 92.5 | 885 | 12 | US-10-282-122A-43572 | Sequence 43572, A |
| 17 | 36 | 90.0 | 6   | 9  | US-09-847-940B-4     | Sequence 4, Appl  |
| 18 | 36 | 90.0 | 6   | 9  | US-09-847-940B-5     | Sequence 5, Appl  |
| 19 | 36 | 90.0 | 6   | 10 | US-09-847-946A-4     | Sequence 4, Appl  |
| 20 | 36 | 90.0 | 6   | 10 | US-09-847-946A-5     | Sequence 5, Appl  |
| 21 | 36 | 90.0 | 6   | 10 | US-09-847-946A-39    | Sequence 39, Appl |
| 22 | 36 | 90.0 | 6   | 10 | US-09-847-946A-40    | Sequence 40, Appl |
| 23 | 36 | 90.0 | 6   | 10 | US-09-847-946A-51    | Sequence 51, Appl |
| 24 | 36 | 90.0 | 6   | 10 | US-09-847-946A-62    | Sequence 62, Appl |
| 25 | 36 | 90.0 | 7   | 10 | US-09-847-946A-55    | Sequence 55, Appl |
| 26 | 36 | 90.0 | 7   | 10 | US-09-847-946A-66    | Sequence 66, Appl |
| 27 | 36 | 90.0 | 8   | 10 | US-09-847-946A-48    | Sequence 48, Appl |
| 28 | 36 | 90.0 | 8   | 10 | US-09-847-946A-56    | Sequence 56, Appl |
| 29 | 36 | 90.0 | 8   | 10 | US-09-847-946A-59    | Sequence 59, Appl |
| 30 | 36 | 90.0 | 8   | 10 | US-09-847-946A-67    | Sequence 67, Appl |
| 31 | 36 | 90.0 | 9   | 10 | US-09-847-946A-47    | Sequence 47, Appl |
| 32 | 36 | 90.0 | 9   | 10 | US-09-847-946A-50    | Sequence 50, Appl |
| 33 | 36 | 90.0 | 9   | 10 | US-09-847-946A-53    | Sequence 53, Appl |
| 34 | 36 | 90.0 | 9   | 10 | US-09-847-946A-54    | Sequence 54, Appl |
| 35 | 36 | 90.0 | 9   | 10 | US-09-847-946A-58    | Sequence 58, Appl |
| 36 | 36 | 90.0 | 9   | 10 | US-09-847-946A-61    | Sequence 61, Appl |
| 37 | 36 | 90.0 | 9   | 10 | US-09-847-946A-64    | Sequence 64, Appl |
| 38 | 36 | 90.0 | 9   | 10 | US-09-847-946A-65    | Sequence 65, Appl |
| 39 | 36 | 90.0 | 10  | 10 | US-09-847-946A-49    | Sequence 49, Appl |
| 40 | 36 | 90.0 | 10  | 10 | US-09-847-946A-52    | Sequence 52, Appl |
| 41 | 36 | 90.0 | 10  | 10 | US-09-847-946A-57    | Sequence 57, Appl |
| 42 | 36 | 90.0 | 10  | 10 | US-09-847-946A-60    | Sequence 60, Appl |
| 43 | 36 | 90.0 | 10  | 10 | US-09-847-946A-63    | Sequence 63, Appl |
| 44 | 36 | 90.0 | 11  | 10 | US-09-847-946A-46    | Sequence 46, Appl |
| 45 | 36 | 90.0 | 147 | 12 | US-10-424-599-199086 | Sequence 199086,  |

## ALIGNMENTS

RESULT 1  
US-09-847-946A-41  
; Sequence 41, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 2

US-09-847-946A-73  
; Sequence 73, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-73

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
|||||  
Db 1 ADWSWA 6

## RESULT 3

US-09-847-946A-77  
; Sequence 77, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 77  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
|||||

Db 1 ADWSWA 6

## RESULT 4

US-09-847-946A-70  
; Sequence 70, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
|||||  
Db 3 ADWSWA 8

## RESULT 5

US-09-847-946A-78  
; Sequence 78, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-78

Query Match 100.0%; Score 40; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

RESULT 6  
US-09-847-946A-69

; Sequence 69, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 69  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

RESULT 7  
US-09-847-946A-72

; Sequence 72, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-72

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

RESULT 8  
US-09-847-946A-75

; Sequence 75, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 3 ADMSWA 8

RESULT 9  
US-09-847-946A-76

; Sequence 76, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-76

; OTHER INFORMATION: sequence  
US-09-847-946A-76

Query Match 100.0%; Score 40; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 2 ADWSWA 7

RESULT 10  
US-09-847-946A-71

; Sequence 71, Application US/09847946A  
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 71

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; US-09-847-946A-71

Query Match 100.0%; Score 40; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 2 ADWSWA 7

RESULT 11  
US-09-847-946A-74

; Sequence 74, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 74

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; US-09-847-946A-74

Query Match 100.0%; Score 40; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 3 ADWSWA 8

RESULT 12  
US-09-847-946A-68

; Sequence 68, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; US-09-847-946A-68

Query Match 100.0%; Score 40; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 3 ADWSWA 8

RESULT 13  
US-10-441-625-17

; Sequence 17, Application US/10441625

; Publication No. US20030203467A1

; GENERAL INFORMATION:

; APPLICANT: Gualfetti, Peter

; APPLICANT: Mitchinson, Colin

; APPLICANT: Phillips, Jay Ian

; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase

; FILE REFERENCE: GC631

; CURRENT APPLICATION NUMBER: US/10/441,625

; CURRENT FILING DATE: 2003-05-19

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Glaciadium roseum (3)

; US-10-441-625-17

Query Match 92.5%; Score 37; DB 12; Length 236;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 63 ADWSWS 68

RESULT 14  
US-10-441-626-17  
; Sequence 17, Application US/10441626  
; Publication No. US20030186418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Phillips, Jay Ian  
; TITLE OF INVENTION: No. US20030186418A1 Variant EGIII-Like Cellulase  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: GC631  
; CURRENT APPLICATION NUMBER: US/10/441, 626  
; CURRENT FILING DATE: 2003-05-19  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Gliocladium roseum (3)  
US-10-441-626-17

Query Match 92.5%; Score 37; DB 14; Length 236;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 63 ADWSWS 68

RESULT 15  
US-09-815-242-5090  
; Sequence 5090, Application US/09815242.  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815, 242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191, 078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206, 848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207, 727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242, 578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253, 625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257, 931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269, 308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5090  
; LENGTH: 885  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 563 ADWAWA 568

Search completed: April 26, 2004, 13:14:32  
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:03:18 ; Search time 39 Seconds  
(without alignments)  
48.541 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvivirus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 37    | 92.5        | 236    | 3 Q8NJY9  | Q8njy9 bionectria   |
| 2          | 37    | 92.5        | 274    | 16 Q8G659 | Q8g659 bifidobacte  |
| 3          | 37    | 92.5        | 375    | 5 Q86K50  | Q86k50 dictyosteli  |
| 4          | 37    | 92.5        | 437    | 16 Q92K30 | Q92k30 rhizobium m  |
| 5          | 37    | 92.5        | 548    | 16 Q92M15 | Q92m15 rhizobium m  |
| 6          | 37    | 92.5        | 581    | 5 Q8MSH3  | Q8msh3 drosophila   |
| 7          | 37    | 92.5        | 597    | 5 Q9VGP2  | Q9vgp2 drosophila   |
| 8          | 37    | 92.5        | 610    | 16 Q86712 | Q86712 streptomyc   |
| 9          | 37    | 92.5        | 885    | 16 Q91389 | Q91389 pseudomonas  |
| 10         | 36    | 90.0        | 173    | 16 Q825E1 | Q825e1 streptomyc   |
| 11         | 36    | 90.0        | 205    | 16 Q9ACR5 | Q9acr5 streptomyc   |
| 12         | 36    | 90.0        | 227    | 4 Q8IXK8  | Q8ixk8 homo sapien  |
| 13         | 36    | 90.0        | 228    | 8 Q7YCU8  | Q7ygu8 sphendon p   |
| 14         | 36    | 90.0        | 242    | 12 Q919K8 | Q919k8 cullex nigri |
| 15         | 36    | 90.0        | 355    | 11 Q8BIT9 | Q8bit9 mus musculu  |
| 16         | 36    | 90.0        | 358    | 10 Q50002 | Q50002 prunus arme  |

|    |    |      |      |           |                     |
|----|----|------|------|-----------|---------------------|
| 17 | 36 | 90.0 | 374  | 16 Q9HZ10 | Q9hz10 pseudomonas  |
| 18 | 36 | 90.0 | 426  | 5 Q86KF9  | Q86kf9 dictyosteli  |
| 19 | 36 | 90.0 | 433  | 16 Q8P4A1 | Q8p4a1 xanthomonas  |
| 20 | 36 | 90.0 | 438  | 16 Q8PFV8 | Q8pfv8 xanthomonas  |
| 21 | 36 | 90.0 | 452  | 4 Q96AB7  | Q96ab7 homo sapien  |
| 22 | 36 | 90.0 | 463  | 5 Q8MMJ0  | Q8mmj0 apis cerana  |
| 23 | 36 | 90.0 | 470  | 12 Q7FE27 | Q7fef27 influenza a |
| 24 | 36 | 90.0 | 477  | 11 Q9CYU6 | Q9cyu6 mus musculu  |
| 25 | 36 | 90.0 | 484  | 4 Q9BTV6  | Q9btv6 homo sapien  |
| 26 | 36 | 90.0 | 605  | 16 Q82MX2 | Q82mx2 streptomyc   |
| 27 | 36 | 90.0 | 686  | 16 Q8FQZ9 | Q8fqz9 corynebacte  |
| 28 | 36 | 90.0 | 861  | 16 Q88NQ1 | Q88nq1 pseudomonas  |
| 29 | 36 | 90.0 | 889  | 16 Q9AAZ6 | Q9aaz6 caulobacter  |
| 30 | 36 | 90.0 | 1005 | 10 Q9XGZ2 | Q9xgz2 arabidopsis  |
| 31 | 36 | 90.0 | 1324 | 16 Q820F9 | Q82of9 streptomyc   |
| 32 | 36 | 90.0 | 5435 | 2 Q9L4X2  | Q9l4x2 streptomyc   |
| 33 | 35 | 87.5 | 527  | 16 Q829Q9 | Q829q9 streptomyc   |
| 34 | 34 | 85.0 | 166  | 4 Q8NBW1  | Q8nbw1 homo sapien  |
| 35 | 34 | 85.0 | 273  | 10 Q94JM4 | Q94jm4 arabidopsis  |
| 36 | 34 | 85.0 | 273  | 10 Q940D6 | Q940d6 arabidopsis  |
| 37 | 34 | 85.0 | 275  | 10 Q65710 | Q65710 arabidopsis  |
| 38 | 34 | 85.0 | 337  | 11 Q80UX8 | Q80ux8 mus musculu  |
| 39 | 34 | 85.0 | 376  | 3 Q9UVL4  | Q9uvl4 penicillium  |
| 40 | 34 | 85.0 | 617  | 10 P93050 | P93050 arabidopsis  |
| 41 | 34 | 85.0 | 1074 | 16 Q8PJ70 | Q8pj70 xanthomonas  |
| 42 | 34 | 85.0 | 1842 | 3 Q96WT6  | Q96wt6 schizosacch  |
| 43 | 34 | 85.0 | 1842 | 3 Q96WT7  | Q96wt7 schizosacch  |
| 44 | 34 | 85.0 | 1842 | 3 Q96WT8  | Q96wt8 schizosacch  |
| 45 | 33 | 82.5 | 49   | 6 Q8SPL6  | Q8spl6 equus cabal  |

#### ALIGNMENTS

RESULT 1

|        |  |      |         |
|--------|--|------|---------|
| Q8NJY9 | PRELIMINARY;   | PRT; | 236 AA. |
| ID     | Q8NJY9   |      |         |
| AC     | Q8NJY9;  |      |         |
| DT     | 01-OCT-2002 (TREMBLrel. 22, Created)                               |      |         |
| DT     | 01-OCT-2002 (TREMBLrel. 22, Last sequence update)                  |      |         |
| DT     | 01-OCT-2003 (TREMBLrel. 25, Last annotation update)                |      |         |
| DE     | Endoglucanase.   |      |         |
| GN     | CEL12C.  |      |         |
| OS     | Bionectria ochroleuca (Glidiocladium roseum).                      |      |         |
| OC     | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;     |      |         |
| OC     | Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.        |      |         |
| OX     | NCBI_TaxID=29856;  |      |         |
| RN     | [1]  |      |         |
| RP     | SEQUENCE FROM N.A.   |      |         |
| RX     | MEDLINE=22067395; PubMed=12073090;                                 |      |         |
| RA     | Goedegebuur F., Fowler T., Phillips J., van der Kley P.,           |      |         |
| RA     | van Solingen P., Dankmeyer L., Power S.D.;                         |      |         |
| RT     | "Cloning and relational analysis of 15 novel fungal endoglucanases |      |         |
| RT     | from family 12 glycosyl hydrolase.";                               |      |         |
| RT     | from family 12 glycosyl hydrolase.";                               |      |         |
| RL     | Curr. Genet. 41:89-98(2002).                                       |      |         |
| DR     | EMBL; AF435065; AAM77708.1;  |      |         |
| DR     | GO; GO:0008810; F:cellulase activity; IEA.                         |      |         |
| DR     | GO; GO:000272; P:polysaccharide catabolism; IEA.                   |      |         |
| DR     | InterPro; IPR008985; Cona_like_1ec_1.                              |      |         |
| DR     | InterPro; IPR002594; Glyco_hydro_12.                               |      |         |
| DR     | Pfam; PF01670; Glyco_hydro_12; 1.                                  |      |         |
| DR     | ProDom; PD004316; Glyco_hydro_12; 1.                               |      |         |
| SQ     | SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;                 |      |         |

Query Match 92.5%; Score 37; DB 3; Length 236;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6  
Db 63 ADWSWS 68

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RESULT 2
Q8G659          PRELIMINARY;      PRT;      274 AA.
ID Q8G659;
AC Q8G659;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Probable dihydroorotate dehydrogenase electron transfer subunit.
GN PYRK OR BL0790.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014701; AAN24605.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008333; FAD binding_6.
DR Pfam; PF00970; FAD_binding_6; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 16; Length 274;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 171 ADWSWS 176

RESULT 3
Q86KS0          PRELIMINARY;      PRT;      375 AA.
ID Q86KS0;
AC Q86KS0;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafarski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox B., Quail M.A., Platzner M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115612; AAO50929.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000581; ILVD_EDD_family.
DR InterPro; IPR006970; PT.
DR Pfam; PF04886; PT; 1.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
KW Hypothetical protein.
```

```
SQ SEQUENCE 375 AA; 41862 MW; EC9A1D744C56856E CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 5; Length 375;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 46 SDWSWA 51

RESULT 4
Q92K30          PRELIMINARY;      PRT;      437 AA.
ID Q92K30;
AC Q92K30;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein R02283.
GN R02283 OR SMC01671.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46862.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 16; Length 437;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 157 ADWNWA 162

RESULT 5
Q92M15          PRELIMINARY;      PRT;      548 AA.
ID Q92M15;
AC Q92M15;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative fatty-acid-CoA ligase protein (EC 6.-.-.-).
GN R02631 OR SMC00741.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
```

RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591791; CAC47210.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003439; ABC transporter.  
DR InterPro; IPR000873; AMP-bind.  
DR Pfam; PF0501; AMP-binding; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
KW ligase; Complete proteome.  
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 235 ADMSWA 240

RESULT 6  
Q8MSH3 PRELIMINARY; PRT; 581 AA.  
AC Q8MSH3;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE GH24640p.  
GN NINAG OR CG6728.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY118818; AAM50678.1; -.  
DR FlyBase; FBgn0037896; ninag.  
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000172; GMC\_oxred.  
DR InterPro; IPR007867; GMC\_oxred\_C.  
DR InterPro; IPR000169; SHprot\_acsite.  
DR Pfam; PF05199; GMC\_oxred\_C; 1.  
DR Pfam; PF00732; GMC\_oxred\_N; 1.  
DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.  
SQ SEQUENCE 581 AA; 63475 MW; A2F13BEB25E496D CRC64;

Query Match 92.5%; Score 37; DB 5; Length 581;  
Best Local Similarity 83.3%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 158 SDMSWA 163

RESULT 7

Q9VGP2 PRELIMINARY; PRT; 597 AA.  
ID Q9VGP2;  
AC Q9VGP2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE CG6728 protein.  
GN NINAG OR CG6728.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Beasley E.M.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertlera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003691; AAF54634.1; -.  
DR FlyBase; FBgn0037896; ninag.  
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000172; GMC\_oxred.  
DR InterPro; IPR007867; GMC\_oxred\_C.  
DR InterPro; IPR000169; SHprot\_acsite.  
DR Pfam; PF05199; GMC\_oxred\_C; 1.  
DR Pfam; PF00732; GMC\_oxred\_N; 1.  
DR PROSITE; PS00624; GMC\_OXRED\_2; 1.  
DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.  
SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFA0902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
Db 158 SDMSWA 163

RESULT 8

086712 PRELIMINARY; PRT; 610 AA.  
AC 086712;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Hypothetical protein SCO6530.  
GN SCO6530 OR SC5C7.15;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;

[1]

RN SEQUENCE FROM N.A.  
RP STRAIN=A3(2) / M145;  
RX MEDLINE=2196410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RL Nature 417:141-147(2002).  
RL EMBL; AL939128; CAA20627.1; -.  
DR PIR; T35222; T35222.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 610;  
Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
Db 83 ADWAWA 88

RESULT 9

091389 PRELIMINARY; PRT; 885 AA.  
ID 091389;  
AC 091389;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Two-component sensor KdpD.  
GN KDPD OR PA1636.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;

[1]

RN SEQUENCE FROM N.A.  
RP STRAIN=ATCC 15692 / PAO1;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Latbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Saiter M.H., Hancock R.E.W., Lory S., Olson M.V.,  
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
CC -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.  
DR EMBL; AE004591; AAG05025.1; -.  
DR PIR; C83441; C83441.  
DR HSSP; P02933; 1JOY.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
DR GO; GO:0006950; P:response to stress; IEA.  
DR GO; GO:0007600; P:sensory perception; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003594; ATPbind\_ATPase.  
DR InterPro; IPR004358; Bact\_sens\_pr\_C.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR005467; His\_kinase.  
DR InterPro; IPR003661; His\_kina\_N.  
DR InterPro; IPR003852; KdpD.  
DR InterPro; IPR006016; Usp\_dom.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR Pfam; PF00512; HisKA; 1.  
DR Pfam; PF02702; KdpD; 1.  
DR Pfam; PF00582; Usp; 1.  
DR PRINTS; PR00344; BCTRLSENSOR.  
DR ProDom; PD011725; KdpD; 1.  
DR SMART; SM00065; GAF; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
DR SMART; SM00388; HisKA; 1.  
DR PROSITE; PS0109; HIS\_KIN; 1.  
KW kinase; phosphorylation; Sensory transduction; Transferase;  
KW Complete proteome.  
SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;  
Best Local Similarity 83.3%; Pred. No. 8.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:|||||  
Db 563 ADWAWA 568

RESULT 10

0825E1 PRELIMINARY; PRT; 173 AA.  
ID 0825E1;  
AC 0825E1;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN SAV7517.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;

[1]

RN SEQUENCE FROM N.A.  
RP STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis: deducing the ability of producing secondary  
RT metabolites";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,



RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:526-531(2003).  
DR EMBL; AP005050; BAC75228.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 173 AA; 18912 MW; 22B26C7D2222CA60 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 173;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
Db 53 ADMEWA 58

## RESULT 11

Q9ACR5 PRELIMINARY; PRT; 205 AA.  
ID Q9ACR5;  
AC Q9ACR5;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Hypothetical protein SCPl.253.  
GN SCPl.253.  
OS Streptomyces coelicolor.  
OG Plasmid SCPl.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=2196410; PubMed=1200953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL590464; CAC36779.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Hypothetical protein; Plasmid; Complete proteome.  
SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5  
Db 10 ADMSW 14

## RESULT 12

Q8IXK8 PRELIMINARY; PRT; 227 AA.  
ID Q8IXK8;  
AC Q8IXK8;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Similar to hypothetical protein BC017335.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC040173; AAH40173.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5  
Db 113 ADMSW 117

## RESULT 13

Q7YGU8 PRELIMINARY; PRT; 228 AA.  
ID Q7YGU8;  
AC Q7YGU8;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit II.  
OS Sphenodon punctatus (Hatteria) (Tuatara).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.  
OX NCBI\_TaxID=8508;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rest J.S., Ast J.C., Austin C.C., Waddell P.J., Tibbetts E.A.,  
Hay J.M., Mindell D.P.;  
RT "Molecular systematics of primary reptilian lineages and the tuatara  
mitochondrial genome.";  
RL Mol. Phylogenet. Evol. 0:0-0(2003).  
DR EMBL; AF534390; AAP42708.1; -.  
KW Mitochondrion.  
SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;

Query Match 90.0%; Score 36; DB 8; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6  
Db 221 DMSWA 225

## RESULT 14

Q919K8 PRELIMINARY; PRT; 242 AA.  
ID Q919K8;  
AC Q919K8;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE CUN068 hypothetical protein.  
GN CUN068.  
OS Culex nigripalpus baculovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
OX NCBI\_TaxID=130556;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Florida1997;  
RX MEDLINE=21488685; PubMed=11602755;  
RA Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,  
Beckel J.J., Rock D.L., Kutish G.F.;  
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";  
RL J. Virol. 75:11157-11165(2001).  
RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=Florida1997;  
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
RA Becnel J.J., Rock D.L., Kutish G.F.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF403738; AAK94146.1; -  
KM Hypothetical protein.  
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6  
|||  
Db 80 DWSWA 84

RESULT 15

Q8BIT9 PRELIMINARY; PRT; 355 AA.  
ID Q8BIT9  
AC Q8BIT9;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Mitochondrial ribosomal protein L41 homolog.  
GN 2810443J12RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK087998; BAC40084.1; -  
DR MGI; MGI:1914478; 2810443J12RIK.  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00400; WD40; 2.  
DR SMART; SM00320; WD40; 4.  
DR PROSITE; PS00678; WD\_REPEATS\_1; 1.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5  
|||  
Db 215 ADWSW 219

Search completed: April 26, 2004, 13:08:48  
Job time : 41 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:04:13 ; Search time 21 Seconds  
(without alignments)  
27.483 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description               |
|------------|-------|-------------|--------------|-------|---------------------------|
| 1          | 37    | 92.5        | 610          | 2     | T35222 hypothetical prote |
| 2          | 37    | 92.5        | 885          | 2     | C83441 two-component sens |
| 3          | 36    | 90.0        | 374          | 2     | B83241 conserved hypothet |
| 4          | 36    | 90.0        | 889          | 2     | E87304 TonB-dependent rec |
| 5          | 34    | 85.0        | 275          | 2     | T05822 hypothetical prote |
| 6          | 34    | 85.0        | 617          | 2     | C84922 probable protein k |
| 7          | 34    | 85.0        | 1842         | 2     | T43409 probable fatty-aci |
| 8          | 34    | 85.0        | 1842         | 2     | T38781 fatty acid synthas |
| 9          | 33    | 82.5        | 132          | 2     | S65785 mel-13a protein -  |
| 10         | 33    | 82.5        | 198          | 2     | B82531 conserved hypothet |
| 11         | 33    | 82.5        | 220          | 2     | D64316 restriction modifi |
| 12         | 33    | 82.5        | 232          | 2     | S58353 CD1b protein - she |
| 13         | 33    | 82.5        | 239          | 2     | D90470 hypothetical prote |
| 14         | 33    | 82.5        | 257          | 2     | D87152 conserved hypothet |
| 15         | 33    | 82.5        | 276          | 2     | B75337 hypothetical prote |
| 16         | 33    | 82.5        | 304          | 2     | F83632 probable cytochrom |
| 17         | 33    | 82.5        | 310          | 2     | JC7853 L-fucose-specific  |
| 18         | 33    | 82.5        | 324          | 2     | AB3548 vegetatible incomp |
| 19         | 33    | 82.5        | 328          | 2     | E72424 oligopeptide ABC t |
| 20         | 33    | 82.5        | 333          | 2     | S47246 gene CDI protein - |
| 21         | 33    | 82.5        | 350          | 2     | S71923 cysteine proteinas |
| 22         | 33    | 82.5        | 368          | 2     | H90998 probable proteinas |
| 23         | 33    | 82.5        | 410          | 2     | D75475 lycopene cyclase - |
| 24         | 33    | 82.5        | 415          | 2     | AE1844 hypothetical prote |
| 25         | 33    | 82.5        | 418          | 2     | AE1460 sugar ABC transpor |
| 26         | 33    | 82.5        | 418          | 2     | AF1097 sugar ABC transpor |
| 27         | 33    | 82.5        | 421          | 2     | T38242 probable phosphata |
| 28         | 33    | 82.5        | 433          | 2     | T31511 hypothetical prote |
| 29         | 33    | 82.5        | 467          | 2     | G82697 hypothetical prote |

|    |    |      |      |   |                            |
|----|----|------|------|---|----------------------------|
| 30 | 33 | 82.5 | 478  | 2 | E89790 6-phospho-beta-glu  |
| 31 | 33 | 82.5 | 479  | 2 | I39953 6-phospho-beta-glu  |
| 32 | 33 | 82.5 | 492  | 2 | S03098 aerolysin precursor |
| 33 | 33 | 82.5 | 529  | 2 | C86958 probable GMP synth  |
| 34 | 33 | 82.5 | 539  | 2 | T15256 hypothetical prote  |
| 35 | 33 | 82.5 | 578  | 2 | C64452 restriction modifi  |
| 36 | 33 | 82.5 | 590  | 2 | S72813 GMP synthase (glut  |
| 37 | 33 | 82.5 | 616  | 2 | C69226 type I restriction  |
| 38 | 33 | 82.5 | 623  | 2 | E75221 type I restriction  |
| 39 | 33 | 82.5 | 765  | 2 | S76795 hypothetical prote  |
| 40 | 33 | 82.5 | 836  | 2 | D82177 conserved hypothet  |
| 41 | 33 | 82.5 | 1202 | 2 | S71424 nitric-oxide synth  |
| 42 | 33 | 82.5 | 1203 | 1 | A47501 nitric-oxide synth  |
| 43 | 33 | 82.5 | 1205 | 1 | A38943 nitric-oxide synth  |
| 44 | 33 | 82.5 | 1329 | 2 | D87226 conserved hypothet  |
| 45 | 33 | 82.5 | 1409 | 2 | S74916 alkaline phosphata  |

## ALIGNMENTS

RESULT 1  
T35222  
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C:Accession: T35222  
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: 221572  
A:Accession: T35222  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-610 <SEE>  
A:Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC5C7.15

Query Match 92.5%; Score 37; DB 2; Length 610;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 83 ADMSWA 88

RESULT 2  
C83441  
two-component sensor KdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: C83441  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brj  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: C83441  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-885 <STO>  
A:Cross-references: GB:AE004591; GB:AE004091; NID:G9947599; PIDN:AAG05025.1; GSPDB:GN0013  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: kdpD; PA1636

Query Match 92.5%; Score 37; DB 2; Length 885;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||:|  
Db 563 ADMAWA 568

## RESULT 3

B83241  
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PA01)  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: B83241  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: B83241  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-374 <STO>  
A/Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001  
C/Genetics:  
A/Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
|||||  
Db 81 DMSWA 85

## RESULT 4

E87304  
TonB-dependent receptor [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C/Accession: E87304  
R/Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; MUID:21173698; PMID:11259647  
A/Accession: E87304  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-889 <STO>  
A/Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148  
C/Genetics:  
A/Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
|||||  
Db 618 ADMSW 622

## RESULT 5

T05822  
hypothetical protein TSK18.170 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999  
C/Accession: T05822  
R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba  
submitted to the Protein Sequence Database, April 1998  
A/Reference number: Z15453

A/Accession: T05822  
A/Molecule type: DNA  
A/Residues: 1-275 <BEV>  
A/Cross-references: EMBL:AL022580  
A/Experimental source: cultivar Columbia; BAC clone TSK18  
C/Genetics:  
A/Map position: 4  
A/Introns: 103/3;  
A/Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
:||||:  
Db 57 SDMSWS 62

## RESULT 6

C84922  
probable protein kinase [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: C84922  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: C84922  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-617 <STO>  
A/Cross-references: GB:AE002093; NID:g4249408; PIDN:AAD13705.1; GSPDB:GN00139  
C/Genetics:  
A/Gene: At2g48010  
A/Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;  
Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||:|:  
Db 500 ADMAWS 505

## RESULT 7

T43409  
probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy  
C/Alternate names: fatty acid synthetase alpha subunit  
C/Species: Schizosaccharomyces pombe  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T43409  
R/Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yan  
J. Cell Biol. 134, 949-961, 1996  
A/Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase and  
A/Reference number: Z22493; MUID:96354912; PMID:8769419  
A/Accession: T43409  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1842 <SAI>  
A/Cross-references: EMBL:D83412; NID:g1199959; PIDN:BAAL1913.1; PID:g1199960  
C/Genetics:  
A/Note: 1sd1+  
C/Superfamily: yeast fatty-acid synthase  
C/Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



QY 1 ADMSWA 6  
:||||  
Db 400 SDWNWA 405

RESULT 8

T38781  
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
C/Accession: T38781  
R/Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A/Reference number: Z21751  
A/Accession: T38781  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1842 <SKE>  
A/Cross-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c  
A/Experimental source: strain 972h-; cosmid c4A8  
C/Genetics:  
A/Gene: SPDB:SPAC4A8.11c  
A/Map position: 1  
C/Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
:||||  
Db 400 SDWNWA 405

RESULT 9

S65785  
mel-13a protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C/Accession: S65785  
R/Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
Biochim. Biophys. Acta 1305, 109-112, 1996  
A/Title: Cloning and characterization of two transcripts generated from the mel-13 gene  
A/Reference number: S65785; MUID:96180310; PMID:8597592  
A/Accession: S65785  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <TET>  
A/Cross-references: EMBL:U35309  
C/Genetics:  
A/Gene: mel-13  
C/Superfamily: mouse mel-13a protein  
C/Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
:||||  
Db 57 SDMSW 61

RESULT 10

B82531  
conserved hypothetical protein XF2666 (imported) - Xylella fastidiosa (strain 9a5c)  
C/Species: Xylella fastidiosa  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000  
C/Accession: B82531  
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347  
A/Note: for a complete list of authors see reference number A59328 below  
A/Accession: B82531  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-198 <SIM>

A/Cross-references: GB:AE004072; GB:AE003849; NID:g2107884; PIDN:AAF85463.1; GSPDB:GN001;  
A/Experimental source: strain 9a5c  
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.  
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki  
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze  
A/Reference number: A59328  
A/Contents: annotation  
C/Genetics:  
A/Gene: XF2666  
C/Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
:||||  
Db 135 DWNWA 139

RESULT 11

D64316  
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii  
C/Species: Methanococcus jannaschii  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2002  
C/Accession: D64316  
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.  
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurest, M.A.  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A/Reference number: A64300; MUID:96337999; PMID:8688087  
A/Accession: D64316  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-220 <BUL>  
A/Cross-references: GB:U67470; GB:L77117; NID:g2826247; PIDN:AAB98113.1; PID:g1592267; T]  
C/Genetics:  
A/Map position: REV127472-126810  
A/Start codon: TTG  
C/Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
:||||  
Db 33 ADMAW 37

RESULT 12

S58353  
Cdlb protein - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C/Accession: S58353

R;Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.  
submitted to the EMBL Data Library, July 1995  
A;Description: The ovine CDI gene family contains at least four CD1B homologues.  
A;Reference number: S58353  
A;Accession: S58353  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-232 <FER>  
A;Cross-references: EMBL:X90567; NID:g945010; PIDN:CAA62187.1; PID:g945011  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:  
Db 156 ADWTW 160

RESULT 13

D90470  
hypothetical protein cySH [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C;Accession: D90470  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: D90470  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-239 <KUR>  
A;Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155  
C;Genetics:  
A;Gene: cySH  
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:  
Db 172 ADWTW 176

RESULT 14

D87152  
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae  
C;Species: Mycobacterium leprae  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C;Accession: D87152  
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho  
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq  
A;Title: Massive gene decay in the leprosy bacillus.  
A;Reference number: A86909; MUID:21128732; PMID:11234002  
A;Accession: D87152  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-257 <STO>  
A;Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147  
C;Genetics:  
A;Gene: ML1945  
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||:  
Db 11 ATWSWA 16

RESULT 15

B75337  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C;Accession: B75337  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I  
, M.; Shen, M.; Yamatchevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: B75337  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-276 <WHI>  
A;Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g6459711  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR1923  
A;Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:  
Db 84 ADMAW 88

Search completed: April 26, 2004, 13:09:21  
Job time : 22 secs



FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;  
Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||||  
DB 453 ADMSW 457

## RESULT 2

NRAM\_IADCH STANDARD; PRT; 470 AA.  
ID\_NRAM\_IADCH

AC 007571;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuraminidase (EC 3.2.1.18).

GN NA.

OS Influenza A virus (strain A/Duck/chabarovsk/1610/72).

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza A viruses; Influenzavirus A.

OX NCBI\_TaxID=38957;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93212520; PubMed=8460490;

RA Saito T., Kawacka Y., Webster R.G.;

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A

RL viruses.";

CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side

CC chains of the host cell surface proteins and from the viral

CC envelope. Such a reaction prevents self-aggregation and facilitate

CC the mobility of the virus to and from the site of infection.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -!- SUBUNIT: Homotetramer.

CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped

CC spike on the surface of the virion.

CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; L06573; AAA43367.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 273 273 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 470 AA; 52070 MW; 169AB89FBE8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||||  
DB 453 ADMSW 457

## RESULT 3

NRAM\_IADH2 STANDARD; PRT; 470 AA.  
ID\_NRAM\_IADH2

AC 007572;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuraminidase (EC 3.2.1.18).

GN NA.

OS Influenza A virus (strain A/Duck/Hokkaido/8/80).

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza A viruses; Influenzavirus A.

OX NCBI\_TaxID=11358;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93212520; PubMed=8460490;

RA Saito T., Kawacka Y., Webster R.G.;

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A

RL viruses.";

CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side

CC chains of the host cell surface proteins and from the viral

CC envelope. Such a reaction prevents self-aggregation and facilitate

CC the mobility of the virus to and from the site of infection.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -!- SUBUNIT: Homotetramer.

CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped

CC spike on the surface of the virion.

CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; L06574; AAA43372.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 273 273 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 453 ADMSW 457

## RESULT 4

NRAM\_IADM2 STANDARD; PRT; 470 AA.  
ID NRAM\_IADM2  
AC Q07573;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Memphis/928/74).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=11367;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; Pubmed=8460490;  
RA Saito T., Kawaoaka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."  
RL Virology 193:868-876(1993).  
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.  
CC -!- SUBUNIT: Homotetramer.  
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.  
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.  
CC -----  
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CC -----  
DR EMBL; L06575; AAA43404.1; -.  
DR HSSP; P06820; 2BAT.  
DR InterPro; IPR001860; Glyco\_hydro\_34.  
DR Pfam; PF00064; neur; 1.  
KW ProDom; PD000431; Glyco\_hydro\_34; 1.  
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.  
FT TRANSMEM 7 ANCHOR (BY SIMILARITY).  
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.  
FT ACT\_SITE 275 275 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
Db 453 ADMSW 457

RESULT 5  
NRAM\_IADU3 STANDARD; PRT; 470 AA.  
ID NRAM\_IADU3  
AC Q07599;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Ukraine/1/63).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=11374;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; Pubmed=8460490;  
RA Saito T., Kawaoaka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."  
RL Virology 193:868-876(1993).  
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.  
CC -!- SUBUNIT: Homotetramer.  
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.  
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.  
CC -----  
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CC -----  
DR EMBL; L06576; AAA16234.1; -.  
DR HSSP; P06820; 2BAT.  
DR InterPro; IPR001860; Glyco\_hydro\_34.  
DR Pfam; PF00064; neur; 1.  
KW ProDom; PD000431; Glyco\_hydro\_34; 1.  
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.  
FT TRANSMEM 7 ANCHOR (BY SIMILARITY).  
FT DOMAIN 38 88 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.  
FT ACT\_SITE 275 275 PROBABLE.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
Db 453 ADMSW 457

RESULT 6  
NRAM\_IAGFN STANDARD; PRT; 470 AA.  
ID NRAM\_IAGFN  
AC Q07574;  
DT 01-FEB-1995 (Rel. 31, Created)



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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; Pubmed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06584; AAA43428.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 7
NRAM_IAHGD STANDARD; PRT; 470 AA.
ID _NRAM_IAHGD
AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
```

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OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; Pubmed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06585; AAA43368.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 8
NRAM_IAHJI STANDARD; PRT; 470 AA.
ID _NRAM_IAHJI
AC Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Equine/Jillin/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; Pubmed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
   viruses."
RL virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06579; AAA43374.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457

RESULT 9
NRAM_IAMAE STANDARD; PRT; 470 AA.
ID_NRAM_IAMAE
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; Pubmed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
   viruses."
RL virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; L06579; AAA43374.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
```

```

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
   viruses."
RL virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; L06586; AAA43369.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457

RESULT 10
NRAM_IATKL STANDARD; PRT; 470 AA.
ID_NRAM_IATKL
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; Pubmed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
   viruses."
RL virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
```

```
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; L06588; AAA43410.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABF1E6B CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457

RESULT 11
MRJ5_APIME STANDARD; PRT; 598 AA.
ID MRJ5_APIME
AC O97432;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S.; Bhattacharya D.; Klaudiny J.; Schmitzova J.; Simuth J.;
RT "The family of major royal jelly proteins and its evolution.";
RL J. Mol. Evol. 49:290-297(1999).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
```

```
CC HONEYBEE QUEEN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -!- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -!- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF004842; AAD01205.1; -.
DR InterPro; IPR003534; RoyalJelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C7E7ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 113 DMSWA 117

RESULT 12
PGLR_PENGR STANDARD; PRT; 376 AA.
ID PGLR_PENGR
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polyalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGL.
OS Penicillium griseoformeum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 6421;
RA Ribon A.B.; Coelho J.L.C.; Barros E.G.; Araujo E.F.;
RT "Cloning and characterization of a gene encoding the
RT endopolylacturonase of Penicillium griseoformeum.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; AF085238; AAC83692.1; -.
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; Pbh1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
```



DR SMART; SM00710; Pbh1; 5.  
 DR PROSITE; PS00502; POLYGALACTURONASE; 1.  
 KW Hydrolase; Glycosidase; Cell wall; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 376 POLYGALACTURONASE.  
 SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC56ED56928 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 :||||:  
 Db 349 SDMSWS 354

## RESULT 13

FAS2\_SCHPO STANDARD; PRT; 1842 AA.  
 AC Q10289; O14163; P78973;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes:  
 DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase  
 DE (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier  
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].  
 GN FAS2 OR LSD1 OR SPAC4A8.11C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE=96354912; PubMed=8769419;  
 RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,  
 RA Hirata A., Yanagida M.;  
 RT "Aberrant mitosis in fission yeast mutants defective in fatty acid  
 RT synthetase and acetyl CoA carboxylase.";  
 RL J. Cell Biol. 134:949-961 (1996).

[2]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=21363051; PubMed=11470243;  
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,  
 RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;  
 RT "Very long-chain fatty-acid-containing phospholipids accumulate in  
 RT fatty acid synthase temperature-sensitive mutant strains of the  
 RT fission yeast Schizosaccharomyces pombe fas2/lcd1.";  
 RL Biochim. Biophys. Acta 1532:223-233 (2001).

[3]  
 SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880 (2002).

[4]  
 RP SEQUENCE OF 1-215 FROM N.A.  
 RA Koken M.H.M., de Rooij J.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

[5]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE=94245730; PubMed=8188691;  
 RA Kaeslin E., Heyer W.-D.;  
 RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand  
 RT exchange in vitro.";  
 RL J. Biol. Chem. 269:14103-14110 (1994).

CC -!- FUNCTION: Fatty acid synthetase catalyzes the formation of  
 CC long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH.  
 CC The alpha subunit contains domains for: acyl carrier protein,  
 CC 3-oxoacyl-[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-  
 CC carrier-protein] synthase. This subunit coordinates the binding  
 CC of the six beta subunits to the enzyme complex.

CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a  
 CC long-chain acyl-CoA + N CO(2) + 2N NADP(+).  
 CC -!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-  
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +  
 CC [acyl-carrier protein].

CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -!- SUBUNIT: [Alpha(6)beta(6)] hexamers of two multifunctional  
 CC subunits (alpha and beta).

CC -!- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM  
 CC OTHER FUNGI.

CC -----  
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CC -----  
 DR EMBL; D83412; BA11913.1; -.  
 DR EMBL; AB013747; BAB62029.1; -.  
 DR EMBL; Z98762; CAB11481.1; -.  
 DR EMBL; U82216; AAB39943.1; -.  
 DR PIR; A54083; A54083.  
 DR PIR; T38781; T38781.  
 DR PIR; T43409; T43409.  
 DR Genedb\_Spombe; SPAC4A8.11C; -.  
 DR InterPro; IPR008278; 4-PPT\_transf.  
 DR InterPro; IPR002582; ACPS.  
 DR InterPro; IPR000794; Ketoadyl\_synth.  
 DR InterPro; IPR004568; Pantetn\_trn.  
 DR InterPro; IPR006162; Pantetn\_S.  
 DR Pfam; PF01648; ACPS; 1.  
 DR Pfam; PF00109; ketoacyl-synt; 1.  
 DR Pfam; PF02801; ketoacyl-synt\_C; 1.  
 DR Prodom; PD004282; ACPS; 1.  
 DR TIGRFAMS; TIGR00556; pantetn\_trn; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; 1.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;  
 KW Transferase; NADP; Phosphopantetheine.  
 FT DOMAIN 1 ?  
 FT DOMAIN 1 ?  
 FT DOMAIN 1 ?  
 FT BINDING 180 1842 BETA-KETOACYL REDUCTASE.  
 FT BINDING 180 180 BETA-KETOACYL SYNTHASE.  
 FT ACT SITE 1262 1262 PHOSPHOPANTHETINE (BY SIMILARITY).  
 FT CONFLICT 107 107 BETA-KETOACYL SYNTHASE (BY SIMILARITY).  
 FT CONFLICT 422 422 S -> A (IN REF. 4).  
 FT CONFLICT 422 422 K -> R (IN REF. 1).

```
SO SEQUENCE 1842 AA; 202168 MW; E4019F2D133EE571 CRC64;
Query Match 85.0%; Score 34; DB 1; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSWA 6
Db 400 SDWMWA 405

RESULT 14
NOS3_SHEEP STANDARD; PRT; 99 AA.
ID NOS3_SHEEP
AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS)
DE (Fragment).
GN NOS3 OR ENOS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT "Effect of hypoxia on the microvasculature of developing fetal
RT brain of sheep: a studies on the expression pattern of
RT constitutive forms of nitric oxide synthase.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
CC -----
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CC -----
CC EMBL; U76738; AAB40705.1; -.
CC HSSP; P29473; IDOC.
CC InterPro; IPR004030; NO_synthase.
CC Pfam; PF02898; NO_synthase; 1.
CC PROSITE; PS60001; NOS; PARTIAL.
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
CC Heme; Multigene family.
CC KW Heme; Multigene family.
CC FT NON_TER 1
CC FT NON_TER 99
CC SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 ADMSW 5
Db 65 ADMAW 69

RESULT 15
Y132_METUA STANDARD; PRT; 220 AA.
ID Y132_METUA
AC Q57596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0132.
DE MJ0132.
GN Methanococcus jannaschii.
OS Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJECU42.
CC -!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
CC (M SUBUNIT).
CC -----
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CC -----
CC EMBL; U67470; AAB98113.1; -.
CC PIR; D64316; D64316.
CC TIGR; MJ0132; -.
CC InterPro; IPR003356; N6_DNA_Mtase.
CC Pfam; PF02384; N6_Mtase; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 220 AA; 25766 MW; 710DDAB4C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Search completed: April 26, 2004, 13:07:56  
Job time : 13 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2004, 13:06:38 ; Search time 23 Seconds  
(without alignments)  
13.468 Million cell updates/sec

Title: US-09-847-940C-6  
Perfect score: 40  
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCrUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 37    | 92.5        | 236    | 4     | US-09-632-570-17     |
| 2          | 37    | 92.5        | 236    | 4     | US-09-632-575-47     |
| 3          | 37    | 92.5        | 938    | 4     | US-09-252-991A-23882 |
| 4          | 36    | 90.0        | 68     | 4     | US-09-252-991A-18367 |
| 5          | 36    | 90.0        | 142    | 4     | US-09-252-991A-31533 |
| 6          | 36    | 90.0        | 174    | 4     | US-09-325-932A-163   |
| 7          | 36    | 90.0        | 225    | 4     | US-09-325-932A-162   |
| 8          | 36    | 90.0        | 242    | 4     | US-09-345-236B-3     |
| 9          | 36    | 90.0        | 378    | 4     | US-09-325-932A-158   |
| 10         | 36    | 90.0        | 445    | 4     | US-09-252-991A-22368 |
| 11         | 36    | 90.0        | 462    | 4     | US-09-252-991A-21704 |
| 12         | 34    | 85.0        | 44     | 3     | US-08-905-223-274    |
| 13         | 33    | 82.5        | 74     | 1     | US-08-379-538-2      |
| 14         | 33    | 82.5        | 136    | 2     | US-08-774-065-2      |
| 15         | 33    | 82.5        | 164    | 4     | US-09-252-991A-23817 |
| 16         | 33    | 82.5        | 218    | 1     | US-08-032-848C-10    |
| 17         | 33    | 82.5        | 218    | 1     | US-08-438-870-10     |
| 18         | 33    | 82.5        | 218    | 2     | US-08-169-948B-34    |
| 19         | 33    | 82.5        | 218    | 2     | US-08-448-873-34     |
| 20         | 33    | 82.5        | 218    | 3     | US-08-382-452D-34    |
| 21         | 33    | 82.5        | 218    | 3     | US-09-216-295-1      |
| 22         | 33    | 82.5        | 218    | 4     | US-08-507-362A-18    |
| 23         | 33    | 82.5        | 218    | 4     | US-09-916-494A-34    |
| 24         | 33    | 82.5        | 218    | 4     | US-09-632-570-1      |
| 25         | 33    | 82.5        | 218    | 4     | US-09-632-575-31     |
| 26         | 33    | 82.5        | 232    | 3     | US-09-146-770-1      |
| 27         | 33    | 82.5        | 232    | 4     | US-09-633-084-1      |

|    |    |      |     |   |                  |                    |
|----|----|------|-----|---|------------------|--------------------|
| 28 | 33 | 82.5 | 232 | 4 | US-10-075-872-1  | Sequence 1, Appli  |
| 29 | 33 | 82.5 | 232 | 4 | US-10-261-997-1  | Sequence 1, Appli  |
| 30 | 33 | 82.5 | 234 | 1 | US-08-032-848C-9 | Sequence 9, Appli  |
| 31 | 33 | 82.5 | 234 | 1 | US-08-438-870-9  | Sequence 9, Appli  |
| 32 | 33 | 82.5 | 234 | 3 | US-09-146-770-3  | Sequence 3, Appli  |
| 33 | 33 | 82.5 | 234 | 3 | US-09-146-770-4  | Sequence 4, Appli  |
| 34 | 33 | 82.5 | 234 | 3 | US-09-216-295-3  | Sequence 3, Appli  |
| 35 | 33 | 82.5 | 234 | 3 | US-09-216-295-4  | Sequence 4, Appli  |
| 36 | 33 | 82.5 | 234 | 4 | US-09-633-084-3  | Sequence 3, Appli  |
| 37 | 33 | 82.5 | 234 | 4 | US-09-633-084-4  | Sequence 4, Appli  |
| 38 | 33 | 82.5 | 234 | 4 | US-10-075-872-3  | Sequence 3, Appli  |
| 39 | 33 | 82.5 | 234 | 4 | US-10-075-872-4  | Sequence 4, Appli  |
| 40 | 33 | 82.5 | 234 | 4 | US-10-261-997-3  | Sequence 3, Appli  |
| 41 | 33 | 82.5 | 234 | 4 | US-10-261-997-4  | Sequence 4, Appli  |
| 42 | 33 | 82.5 | 234 | 4 | US-09-632-570-3  | Sequence 3, Appli  |
| 43 | 33 | 82.5 | 234 | 4 | US-09-632-570-4  | Sequence 4, Appli  |
| 44 | 33 | 82.5 | 234 | 4 | US-09-632-575-33 | Sequence 33, Appli |
| 45 | 33 | 82.5 | 234 | 4 | US-09-632-575-34 | Sequence 34, Appli |

ALIGNMENTS

RESULT 1  
US-09-632-570-17  
Sequence 17, Application US/09632570  
Patent No. 6623949  
GENERAL INFORMATION:  
APPLICANT: Gualfetti, Peter  
APPLICANT: Mitchinson, Colin  
APPLICANT: Phillips, Jay Ian  
TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase  
FILE REFERENCE: GC631  
CURRENT APPLICATION NUMBER: US/09/632,570  
CURRENT FILING DATE: 2000-08-04  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Gliocladium roseum (3)  
US-09-632-570-17

Query Match 92.5%; Score 37; DB 4; Length 236;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6  
Db 63 ADWSWS 68

RESULT 2  
US-09-632-575-47  
Sequence 47, Application US/09632575  
Patent No. 6635465  
GENERAL INFORMATION:  
APPLICANT: Gualfetti, Peter  
APPLICANT: Mitchinson, Colin  
APPLICANT: Ropp, Traci M.  
TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding  
FILE REFERENCE: GC629  
CURRENT APPLICATION NUMBER: US/09/632,575  
CURRENT FILING DATE: 2000-08-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 47  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Gliocladium roseum (3)  
US-09-632-575-47

Query Match 92.5%; Score 37; DB 4; Length 236;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSWA 6  
Db 63 ADWSWS 68

## RESULT 3

US-09-252-991A-23882  
; Sequence 23882, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23882  
; LENGTH: 938  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23882

Query Match 92.5%; Score 37; DB 4; Length 938;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSWA 6  
Db 581 ADWAWA 586

## RESULT 4

US-09-252-991A-18367  
; Sequence 18367, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18367  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DWSWA 6  
Db 2 DWSWA 6

## RESULT 5

US-09-252-991A-31533  
; Sequence 31533, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31533  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
Db 94 ADMSW 98

## RESULT 6

US-09-325-932A-163  
; Sequence 163, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 163  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Eucalyptus grandis  
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
Db 109 ADMSW 113

## RESULT 7

US-09-325-932A-162  
; Sequence 162, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 162  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Eucalyptus grandis  
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 100 ADMSW 104

## RESULT 8

US-09-345-236B-3  
; Sequence 3, Application US/09345236B  
; Patent No. 6521454  
; GENERAL INFORMATION:

; APPLICANT: Becnel, James J.  
; APPLICANT: Tuku, Fukuda  
; APPLICANT: Moser, Bettina  
; APPLICANT: Cockburn, Andrew  
; APPLICANT: White, Susan E.  
; APPLICANT: Undeen, Albert H.  
; TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal  
; TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates  
; FILE REFERENCE: 21042.0004  
; CURRENT APPLICATION NUMBER: US/09/345,236B  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: mosquito baculovirus  
US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
Db 80 DMSWA 84

## RESULT 9

US-09-325-932A-158  
; Sequence 158, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of forestry plant devel  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 158  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Eucalyptus grandis  
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

Db 128 ADMSW 132

## RESULT 10

US-09-252-991A-22368  
; Sequence 22368, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22368  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
Db 304 DMSWA 308

## RESULT 11

US-09-252-991A-21704  
; Sequence 21704, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21704  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
Db 169 DMSWA 173

## RESULT 12

US-08-905-223-274  
; Sequence 274, Application US/08905223  
; Patent No. 6222029  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste D.  
; APPLICANT: Duclert, Aymeric

APPLICANT: Lacroix, Bruno  
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Knobb, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 274:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -26...-1  
IDENTIFICATION METHOD: Von Heijne matrix  
OTHER INFORMATION: score 9.6  
OTHER INFORMATION: seq WLIALASWSWALC/RI  
US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;  
Best Local Similarity 83.3%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
Db 19 ASWSWA 24

RESULT 13  
US-08-379-538-2  
Sequence 2, Application US/08379538  
Patent No. 5804554  
GENERAL INFORMATION:  
APPLICANT: Volkman, Robert A.  
APPLICANT: Saccomano, Nicholas A.  
APPLICANT: Nason II, Deane M.  
APPLICANT: Heck, Steven D.  
APPLICANT: Ronau, Robert T.  
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES  
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pfizer Inc  
STREET: 235 East 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,538  
FILING DATE: 3-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887073  
FILING DATE: 21-MAY-1992  
APPLICATION NUMBER: PCT/US93/03921  
FILING DATE: 30-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Zielinski, Bryan  
REGISTRATION NUMBER: 34,462  
REFERENCE/DOCKET NUMBER: PC8175A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 573-4585  
TELEFAX: (212) 573-1939  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 74 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
ORGANISM: Filistata hibernalis  
TISSUE TYPE: venom  
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;  
Best Local Similarity 80.0%; Pred. No. 11e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6  
Db 52 DWSWS 56

RESULT 14  
US-08-774-065-2  
Sequence 2, Application US/08774065  
Patent No. 5989899  
GENERAL INFORMATION:  
APPLICANT: Bower, Benjamin  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Larens, Edmund  
APPLICANT: Ward, Michael  
TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS  
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND  
TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: GENENCOR INTERNATIONAL  
STREET: 925 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,065  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Glaister, Debra J.  
 REGISTRATION NUMBER: 33,888  
 REFERENCE/DOCKET NUMBER: GC368  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-846-7620  
 TELEFAX: 415-845-6504  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 136 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
 Db 62 ADWQWS 67

RESULT 15  
 US-09-252-991A-23817  
 ; Sequence 23817, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 23817  
 ; LENGTH: 164  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
 Db 132 AGWSWA 137

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 Job time : 24 secs



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OM protein - protein search, using sw model

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Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADWSWA 6

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pending Patents AA Main:\*

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32: /cgn2\_6/ptodata/2/paa/US107\_COMB.pep.\*  
33: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1  | 40 | 100.0 | 6   | 20 | US-09-643-260-6      | Sequence 6, Appli |
| 2  | 40 | 100.0 | 6   | 23 | US-09-847-946A-41    | Sequence 41, Appl |
| 3  | 40 | 100.0 | 6   | 23 | US-09-847-946A-73    | Sequence 73, Appl |
| 4  | 40 | 100.0 | 7   | 23 | US-09-847-946A-77    | Sequence 77, Appl |
| 5  | 40 | 100.0 | 8   | 23 | US-09-847-946A-70    | Sequence 70, Appl |
| 6  | 40 | 100.0 | 8   | 23 | US-09-847-946A-78    | Sequence 78, Appl |
| 7  | 40 | 100.0 | 9   | 23 | US-09-847-946A-69    | Sequence 69, Appl |
| 8  | 40 | 100.0 | 9   | 23 | US-09-847-946A-72    | Sequence 72, Appl |
| 9  | 40 | 100.0 | 9   | 23 | US-09-847-946A-75    | Sequence 75, Appl |
| 10 | 40 | 100.0 | 9   | 23 | US-09-847-946A-76    | Sequence 76, Appl |
| 11 | 40 | 100.0 | 10  | 23 | US-09-847-946A-71    | Sequence 71, Appl |
| 12 | 40 | 100.0 | 10  | 23 | US-09-847-946A-74    | Sequence 74, Appl |
| 13 | 40 | 100.0 | 11  | 23 | US-09-847-946A-68    | Sequence 68, Appl |
| 14 | 37 | 92.5  | 33  | 1  | PCT-US01-01321-1549  | Sequence 1549, Ap |
| 15 | 37 | 92.5  | 103 | 16 | US-09-284-327A-45    | Sequence 45, Appl |
| 16 | 37 | 92.5  | 236 | 1  | PCT-US00-33878-47    | Sequence 47, Appl |
| 17 | 37 | 92.5  | 236 | 15 | US-09-147-729-16     | Sequence 16, Appl |
| 18 | 37 | 92.5  | 236 | 15 | US-09-284-327-22     | Sequence 22, Appl |
| 19 | 37 | 92.5  | 236 | 16 | US-09-284-327A-22    | Sequence 22, Appl |
| 20 | 37 | 92.5  | 236 | 18 | US-09-470-832-47     | Sequence 47, Appl |
| 21 | 37 | 92.5  | 236 | 20 | US-09-632-426-17     | Sequence 17, Appl |
| 22 | 37 | 92.5  | 236 | 30 | US-10-441-625-17     | Sequence 17, Appl |
| 23 | 37 | 92.5  | 236 | 30 | US-10-441-626-17     | Sequence 17, Appl |
| 24 | 37 | 92.5  | 247 | 33 | US-60-142-896-1376   | Sequence 1376, Ap |
| 25 | 37 | 92.5  | 247 | 33 | US-60-143-992-1434   | Sequence 1434, Ap |
| 26 | 37 | 92.5  | 597 | 20 | US-09-614-150-14697  | Sequence 14697, A |
| 27 | 37 | 92.5  | 597 | 20 | US-09-614-150A-14697 | Sequence 14697, A |
| 28 | 37 | 92.5  | 597 | 22 | US-09-791-537-32630  | Sequence 32630, A |
| 29 | 37 | 92.5  | 597 | 33 | US-60-173-464-12020  | Sequence 12020, A |
| 30 | 37 | 92.5  | 597 | 33 | US-60-191-637-14738  | Sequence 14738, A |
| 31 | 37 | 92.5  | 597 | 33 | US-60-191-681-11618  | Sequence 11618, A |
| 32 | 37 | 92.5  | 885 | 1  | PCT-US02-03987-5090  | Sequence 5090, Ap |
| 33 | 37 | 92.5  | 885 | 23 | US-09-815-242-5090   | Sequence 5090, Ap |
| 34 | 37 | 92.5  | 885 | 26 | US-10-072-851-5090   | Sequence 5090, Ap |
| 35 | 37 | 92.5  | 885 | 28 | US-10-282-122A-43572 | Sequence 43572, A |
| 36 | 37 | 92.5  | 885 | 33 | US-60-253-625-2729   | Sequence 2729, Ap |
| 37 | 37 | 92.5  | 885 | 33 | US-60-257-931-3557   | Sequence 3557, Ap |
| 38 | 37 | 92.5  | 885 | 33 | US-60-269-308-4579   | Sequence 4579, Ap |
| 39 | 37 | 92.5  | 938 | 29 | US-10-366-683-23882  | Sequence 23882, A |
| 40 | 37 | 92.5  | 938 | 30 | US-10-419-128-23882  | Sequence 23882, A |
| 41 | 36 | 90.0  | 6   | 20 | US-09-643-260-4      | Sequence 4, Appli |
| 42 | 36 | 90.0  | 6   | 20 | US-09-643-260-5      | Sequence 5, Appli |
| 43 | 36 | 90.0  | 6   | 23 | US-09-847-940B-4     | Sequence 4, Appli |
| 44 | 36 | 90.0  | 6   | 23 | US-09-847-940B-5     | Sequence 5, Appli |
| 45 | 36 | 90.0  | 6   | 23 | US-09-847-946A-4     | Sequence 4, Appli |

ALIGNMENTS

RESULT 1  
US-09-643-260-6  
Sequence 6, Application US/09643260  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: Inhibition of NF-kappa B Activation by Blockade of IKK  
FILE REFERENCE: 44574-5066-US  
CURRENT APPLICATION NUMBER: US/09/643, 260  
CURRENT FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 60/201, 261  
PRIOR FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutant  
US-09-643-260-6

Query Match 100.0%; Score 40; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
|||  
Db 1 ADMSWA 6

## RESULT 2

US-09-847-946A-41  
; Sequence 41, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
|||  
Db 1 ADMSWA 6

## RESULT 3

US-09-847-946A-73  
; Sequence 73, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 73  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence

US-09-847-946A-73

Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
|||  
Db 1 ADMSWA 6

## RESULT 4

US-09-847-946A-77  
; Sequence 77, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 77  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6  
|||  
Db 1 ADMSWA 6

## RESULT 5

US-09-847-946A-70  
; Sequence 70, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence

OTHER INFORMATION: sequence  
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 3 ADMSWA 8

## RESULT 6

US-09-847-946A-78  
; Sequence 78, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-78

Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 1 ADMSWA 6

## RESULT 7

US-09-847-946A-69  
; Sequence 69, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 69  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 1 ADMSWA 6

## RESULT 8

US-09-847-946A-72  
; Sequence 72, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-72

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 1 ADMSWA 6

## RESULT 9

US-09-847-946A-75  
; Sequence 75, Application US/09847946A  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 3 ADWSWA 8

RESULT 10  
US-09-847-946A-76  
Sequence 76, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 76  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-76

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 2 ADWSWA 7

RESULT 11  
US-09-847-946A-71  
Sequence 71, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 71  
LENGTH: 10  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-71

Query Match 100.0%; Score 40; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 2 ADWSWA 7

RESULT 12  
US-09-847-946A-74  
Sequence 74, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 74  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-74

Query Match 100.0%; Score 40; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
| | | | |  
Db 3 ADWSWA 8

RESULT 13  
US-09-847-946A-68  
Sequence 68, Application US/09847946A  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 11  
TYPE: PRT



TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
 OTHER INFORMATION: sequence  
 US-09-847-946A-68

Query Match 100.0%; Score 40; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
 Db 3 ADWSWA 8

RESULT 14  
 PCT-US01-01321-1549  
 Sequence 1549, Application PC/TUS0101321  
 GENERAL INFORMATION:  
 APPLICANT: Human Genome Sciences, Inc., et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PC011PCT  
 CURRENT APPLICATION NUMBER: PCT/US01/01321  
 CURRENT FILING DATE: 2001-01-17  
 NUMBER OF SEQ ID NOS: 2181  
 SOFTWARE: Patentln Ver. 2.0  
 SEQ ID NO 1549  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 PCT-US01-01321-1549

Query Match 92.5%; Score 37; DB 1; Length 33;  
 Best Local Similarity 83.3%; Pred. No. 6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6  
 Db 9 ADWTWA 14

RESULT 15  
 US-09-284-327A-45  
 Sequence 45, Application US/09284327A  
 GENERAL INFORMATION:  
 APPLICANT: Bower, Benjamin S.  
 APPLICANT: Fowler, Timothy  
 APPLICANT: Phillips, Jay I.  
 TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding  
 TITLE OF INVENTION: Such Enzymes and Methods for Producing Such Enzymes  
 FILE REFERENCE: GC516-2-US  
 CURRENT APPLICATION NUMBER: US/09/284,327A  
 CURRENT FILING DATE: 1999-04-10  
 PRIOR APPLICATION NUMBER: PCT/US98/26552  
 PRIOR FILING DATE: 1998-12-14  
 NUMBER OF SEQ ID NOS: 68  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 45  
 LENGTH: 103  
 TYPE: PRT  
 ORGANISM: Gliocladium roseum  
 US-09-284-327A-45

Query Match 92.5%; Score 37; DB 16; Length 103;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 29 ADWSWS 34

Search completed: April 26, 2004, 13:13:10  
 Job time : 182 secs

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